

SEQUENCE LISTING

<110> E.I. duPont de Nemours and Company Inc.
Meyer, Knut
Dhugga, Kanwarpal

<120> Method to Produce para-Hydroxybenzoic Acid in the Stem Tissue of
a Plant

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<220>		
<223> Primer		
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<223> Primer		
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<210> 27
 <211> 3552
 <212> DNA
 <213> artificial sequence

 <220>
 <223> Chimeric gene. C4H promoter operably linked to HCHL coding sequence.

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<210> 28

<211> 3570

<212> DNA

<213> artificial sequence

<220>

<223> Chimeric gene. 4CL1 promoter operably linked to HCHL coding sequence.

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<211> 3536
<212> DNA
<213> artificial sequence

<220>
<223> Chimeric gene. C3H promoter operably linked to HCHL coding sequence.

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<211> 1007

<212> PRT

<213> Zea mays

<400> 34

Met Met Glu Ser Ala Ala Ala Gln Ser Cys Ala Ala Cys Gly Asp Asp	
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20	30

Leu Asp Glu Asp Ala Ala Glu Gly Arg Thr Thr Cys Ala Arg Cys Gly	
35	40
35	45

Gly Asp Tyr Ala Ala Ile Asn Pro Ala Arg Ala Ser Glu Gly Thr Glu	
50	55
50	60

Ala Glu Glu Glu Val Val Glu Asn His His Thr Ala Gly Gly Leu Arg	
65	70
65	75
65	80

Glu Arg Val Thr Met Gly Ser His Leu Asn Asp Arg Gln Asp Glu Val	
85	90
85	95

Ser His Ala Arg Thr Met Ser Ser Leu Ser Gly Ile Gly Ser Glu Leu	
100	105
100	110

Asn Asp Glu Ser Gly Lys Pro Ile Trp Lys Asn Arg Val Glu Ser Trp	
115	120
115	125

Lys Glu Lys Lys Asn Glu Lys Lys Ala Ser Ala Lys Lys Thr Ala Ala	
130	135
130	140

Lys Ala Gln Pro Pro Pro Val Glu Glu Gln Ile Met Asp Glu Lys Asp	
145	150
145	155
145	160

Leu Thr Asp Ala Tyr Glu Pro Leu Ser Arg Val Ile Pro Ile Ser Lys	
165	170
165	175

Asn Lys Leu Thr Pro Tyr Arg Ala Val Ile Ile Met Arg Leu Ile Val	
180	185
180	190

Leu Gly Leu Phe Phe His Tyr Arg Ile Thr Asn Pro Val Asn Ser Ala
195 200 205

Phe Gly Leu Trp Met Thr Ser Val Ile Cys Glu Ile Trp Phe Gly Phe
210 215 220

Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Tyr Pro Ile Asn Arg Glu
225 230 235 240

Thr Tyr Val Asp Arg Leu Ile Ala Arg Tyr Gly Asp Gly Glu Ser
245 250 255

Gly Leu Ala Pro Val Asp Phe Phe Val Ser Thr Val Asp Pro Leu Lys
260 265 270

Glu Pro Pro Leu Ile Thr Ala Asn Thr Val Leu Ser Ile Leu Ala Val
275 280 285

Asp Tyr Pro Val Glu Lys Ile Ser Cys Tyr Val Ser Asp Asp Gly Ser
290 295 300

Ala Met Leu Thr Phe Glu Ser Leu Ala Glu Thr Ala Glu Tyr Ala Arg
305 310 315 320

Lys Trp Val Pro Phe Cys Lys Tyr Ala Ile Glu Pro Arg Ala Pro
325 330 335

Glu Phe Tyr Phe Ser Gln Lys Ile Asp Tyr Leu Lys Asp Lys Ile His
340 345 350

Pro Ser Phe Val Lys Glu Arg Arg Ala Met Lys Arg Asp Tyr Glu Glu
355 360 365

Tyr Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Thr Pro
370 375 380

Asp Glu Gly Trp Ile Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn
385 390 395 400

Pro Arg Asp His Pro Gly Met Ile Gln Val Phe Leu Gly Glu Thr Gly
405 410 415

Ala Arg Asp Phe Asp Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser
420 425 430

Arg Glu Lys Arg Pro Gly Tyr Gln His His Lys Lys Ala Gly Ala Met
435 440 445

Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn Ala Pro Tyr Ile
450 455 460

Leu Asn Leu Asp Cys Asp His Tyr Val Asn Asn Ser Lys Ala Val Arg

465	470	475	480
Glu Ala Met Cys Phe Met Met Asp Pro Thr Val Gly Arg Asp Val Cys 485		490	495
Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg Ser Asp Arg 500	505		510
Tyr Ala Asn Arg Asn Val Val Phe Phe Asp Val Asn Met Lys Gly Leu 515	520	525	
Asp Gly Leu Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Cys Phe Asn 530	535	540	
Arg Gln Ala Leu Tyr Gly Tyr Gly Pro Pro Ser Leu Pro Ala Leu Pro 545	550	555	560
Lys Ser Ser Ile Cys Ser Trp Cys Cys Cys Cys Pro Lys Lys Lys 565	570		575
Val Glu Arg Ser Glu Arg Glu Ile Asn Arg Asp Ser Arg Arg Glu Asp 580	585		590
Leu Glu Ser Ala Ile Phe Asn Leu Arg Glu Ile Asp Asn Tyr Asp Glu 595	600	605	
Tyr Glu Arg Ser Met Leu Ile Ser Gln Met Ser Phe Glu Lys Ser Phe 610	615	620	
Gly Leu Ser Ser Val Phe Ile Glu Ser Thr Leu Met Glu Asn Gly Gly 625	630	635	640
Val Pro Glu Ser Ala Asn Pro Ser Thr Leu Ile Lys Glu Ala Ile His 645	650		655
Val Ile Ser Cys Gly Tyr Glu Glu Lys Thr Glu Trp Gly Lys Glu Ile 660	665	670	
Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys 675	680	685	
Met His Cys Arg Gly Trp Arg Ser Ile Tyr Cys Met Pro Val Arg Pro 690	695	700	
Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu His Gln 705	710	715	720
Val Leu Arg Trp Ala Leu Val Ser Val Glu Ile Phe Phe Ser Arg His 725	730	735	
Cys Pro Leu Trp Tyr Gly Tyr Gly Gly Arg Leu Lys Trp Leu Gln 740	745	750	

Arg Leu Ser Tyr Ile Asn Thr Ile Val Tyr Pro Phe Thr Ser Leu Pro
 755 760 765
 Leu Val Ala Tyr Cys Cys Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys
 770 775 780
 Phe Ile Ile Pro Thr Leu Ser Asn Ala Ala Thr Ile Trp Phe Leu Gly
 785 790 795 800
 Leu Phe Met Ser Ile Ile Val Thr Ser Val Leu Glu Leu Arg Trp Ser
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 Gly Ile Gly Ile Glu Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile
 820 825 830
 Gly Gly Val Ser Ala His Leu Phe Ala Val Phe Gln Gly Ile Leu Lys
 835 840 845
 Met Ile Ala Gly Leu Asp Thr Asn Phe Thr Val Thr Ala Lys Ala Thr
 850 855 860
 Asp Asp Thr Glu Phe Gly Glu Leu Tyr Leu Phe Lys Trp Thr Thr Val
 865 870 875 880
 Leu Ile Pro Pro Thr Ser Ile Leu Val Leu Asn Leu Val Gly Val Val
 885 890 895
 Ala Gly Phe Ser Ala Ala Leu Asn Ser Gly Tyr Glu Ser Trp Gly Pro
 900 905 910
 Leu Phe Gly Lys Val Phe Phe Ala Met Trp Val Ile Met His Leu Tyr
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 Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg Thr Pro Thr Ile
 930 935 940
 Val Val Leu Trp Ser Val Leu Leu Ala Ser Val Phe Ser Leu Leu Trp
 945 950 955 960
 Val Lys Ile Asp Pro Phe Val Gly Gly Thr Glu Thr Val Asn Thr Asn
 965 970 975
 Asn Cys Asn Thr His Leu Leu Ile His His Arg Ser Ala Ala Val Val
 980 985 990
 Pro Arg Arg Thr Cys Phe Trp Cys Cys Lys Arg Gly Leu Pro Ala
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 <211> 3443
 <212> DNA

<213> Zea mays

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		ctcgacaaac cggAACGAGC tggtgcgtat ccggggccac gaggaccca agccgctgcg	180
		ggcgtgagc gggcagggtgt gcgagatatg cggcgtcagag gtcggctca cgggtggacgg	240
		cgacctttc gtcgcctgca acgagtgcgg cttccccgtg tgccggccct gctacgagta	300
		cgagcgccgg gagggcacgc agaactgccc ccagtcaag acgcgtaca agcgcctcaa	360
		ggggagcccgg agggttgccg gggacgtga cgaggaggac atcgacgacc tggagcacga	420
		gttcaacatc gacgacgaga atcagcagag gcagctggag ggcaacatgc agaacagcca	480
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		cggcaacaac accccgcaga tcccgcccat catcaccggc tcccgctccg tgccggtgag	600
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acaatttaga aattttgtaa ggttgggtg tctgtatgt tatggtaacc agaattgtcg	3360
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 <211> 1052
 <212> PRT
 <213> Zea mays

<400> 36

Met Glu Ala Ser Ala Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu
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Leu Val Leu Ile Arg Gly His Glu Asp Pro Lys Pro Leu Arg Ala Leu
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Ser Gly Gln Val Cys Glu Ile Cys Gly Asp Glu Val Gly Leu Thr Val
 35 40 45

Asp Gly Asp Leu Phe Val Ala Cys Asn Glu Cys Gly Phe Pro Val Cys
 50 55 60

Arg Pro Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro
 65 70 75 80

Gln Cys Lys Thr Arg Tyr Lys Arg Leu Lys Gly Ser Pro Arg Val Ala
 85 90 95

Gly Asp Asp Asp Glu Glu Asp Ile Asp Asp Leu Glu His Glu Phe Asn
 100 105 110

Ile Asp Asp Glu Asn Gln Gln Arg Gln Leu Glu Gly Asn Met Gln Asn
 115 120 125

Ser Gln Ile Thr Glu Ala Met Leu His Gly Arg Met Ser Tyr Gly Arg
 130 135 140

Gly Pro Asp Asp Gly Asp Gly Asn Asn Thr Pro Gln Ile Pro Pro Ile
 145 150 155 160

Ile Thr Gly Ser Arg Ser Val Pro Val Ser Gly Glu Phe Pro Ile Thr
 165 170 175

Asn Gly Tyr Gly His Gly Glu Val Ser Ser Ser Leu His Lys Arg Ile
 180 185 190

His Pro Tyr Pro Val Ser Glu Pro Gly Ser Ala Lys Trp Asp Glu Lys
 195 200 205

Lys Glu Val Ser Trp Lys Glu Arg Met Asp Asp Trp Lys Ser Lys Gln
 210 215 220

Gly Ile Leu Gly Gly Ala Asp Pro Glu Asp Met Asp Ala Asp Val
 225 230 235 240

Ala Leu Asn Asp Glu Ala Arg Gln Pro Leu Ser Arg Lys Val Ser Ile
 245 250 255

Ala Ser Ser Lys Val Asn Pro Tyr Arg Met Val Ile Val Val Arg Leu
 260 265 270

Val Val Leu Ala Phe Phe Leu Arg Tyr Arg Ile Leu His Pro Val Pro
 275 280 285

Asp Ala Ile Gly Leu Trp Leu Val Ser Ile Ile Cys Glu Ile Trp Phe
 290 295 300

Ala Ile Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Phe Pro Ile Asp
 305 310 315 320

Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Tyr Glu Arg Glu Gly
325 330 335

Glu Pro Ser Leu Leu Ser Ala Val Asp Leu Phe Val Ser Thr Val Asp
340 345 350

Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Val Leu Ser Ile
355 360 365

Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser Cys Tyr Val Ser Asp
370 375 380

Asp Gly Ala Ser Met Leu Thr Phe Glu Ser Leu Ser Glu Thr Ala Glu
385 390 395 400

Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys Phe Gly Ile Glu Pro
405 410 415

Arg Ala Pro Glu Phe Tyr Phe Ser Leu Lys Val Asp Tyr Leu Lys Asp
420 425 430

Lys Val Gln Pro Thr Phe Val Gln Glu Arg Arg Ala Met Lys Arg Glu
435 440 445

Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Met
450 455 460

Lys Val Pro Ala Glu Gly Trp Ile Met Lys Asp Gly Thr Pro Trp Pro
465 470 475 480

Gly Asn Asn Thr Arg Asp His Pro Gly Met Ile Gln Val Phe Leu Gly
485 490 495

His Ser Gly Gly His Asp Thr Glu Gly Asn Glu Leu Pro Arg Leu Val
500 505 510

Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln His His Lys Lys Ala
515 520 525

Gly Ala Met Asn Ala Leu Ile Arg Val Ser Ala Val Leu Thr Asn Ala
530 535 540

Pro Phe Met Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys
545 550 555 560

Ala Ile Arg Glu Ala Met Cys Phe Leu Met Asp Pro Gln Val Gly Arg
565 570 575

Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Val
580 585 590

His Asp Arg Tyr Ala Asn Arg Asn Thr Val Phe Phe Asp Ile Asn Met

595	600	605
Lys Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr Val	Gly Thr Gly Cys	
610 615	620	
Val Phe Arg Arg Gln Ala Leu Tyr Gly Tyr Asn Pro	Pro Lys Gly Pro	640
625 630	635	
Lys Arg Pro Lys Met Val Thr Cys Asp Cys Cys Pro	Cys Phe Gly Arg	655
645 650	655	
Lys Lys Arg Lys His Ala Lys Asp Gly Leu Pro Glu	Gly Thr Ala Asp	
660 665	670	
Met Gly Val Asp Ser Asp Lys Glu Met Leu Met Ser	His Met Asn Phe	
675 680	685	
Glu Lys Arg Phe Gly Gln Ser Ala Ala Phe Val Thr	Ser Thr Leu Met	
690 695	700	
Glu Glu Gly Val Pro Pro Ser Ser Pro Ala Ala Leu	Leu Lys	720
705 710	715	
Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp	Lys Thr Asp Trp	
725 730	735	
Gly Leu Glu Leu Gly Trp Ile Tyr Gly Ser Ile Thr	Glu Asp Ile Leu	
740 745	750	
Thr Gly Phe Lys Met His Cys Arg Gly Trp Arg Ser	Val Tyr Cys Met	
755 760	765	
Pro Lys Arg Ala Ala Phe Lys Gly Ser Ala Pro Ile	Asn Leu Ser Asp	
770 775	780	
Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly Ser	Val Glu Ile Phe	
785 790	795	800
Phe Ser Arg His Ser Pro Leu Leu Tyr Gly Tyr Lys	Asn Gly Asn Leu	
805 810	815	
Lys Trp Leu Glu Arg Phe Ala Tyr Ile Asn Thr Thr	Ile Tyr Pro Phe	
820 825	830	
Thr Ser Leu Pro Leu Leu Ala Tyr Cys Thr Leu Pro	Ala Val Cys Leu	
835 840	845	
Leu Thr Gly Lys Phe Ile Met Pro Ser Ile Ser Thr	Phe Ala Ser Leu	
850 855	860	
Phe Phe Ile Ala Leu Phe Met Ser Ile Phe Ala Thr	Gly Ile Leu Glu	880
865 870	875	

Met Arg Trp Ser Gly Val Ser Ile Glu Glu Trp Trp Arg Asn Glu Gln
 885 890 895
 Phe Trp Val Ile Gly Gly Val Ser Ala His Leu Phe Ala Val Val Gln
 900 905 910
 Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn Phe Thr Val Thr
 915 920 925
 Ser Lys Ala Thr Gly Asp Glu Asp Asp Glu Phe Ala Glu Leu Tyr Ala
 930 935 940
 Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu Ile Ile
 945 950 955 960
 Asn Val Ile Gly Val Val Ala Gly Ile Ser Asp Ala Ile Asn Asn Gly
 965 970 975
 Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp
 980 985 990
 Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln
 995 1000 1005
 Asn Arg Thr Pro Thr Val Val Ile Trp Ser Ile Leu Leu Ala
 1010 1015 1020
 Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Ile Val
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 Arg Thr Lys Gly Pro Asp Val Arg Gln Cys Gly Ile Asn Cys
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 <211> 3191
 <212> DNA
 <213> Oryza sativa

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<210> 38

<211> 1063

<212> PRT

<213> Oryza sativa

<400> 38

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Thr	Cys	Arg	val	cys	Gly	Glu	Glu	val	Ala	Ala	Arg	Glu	Asp	Gly	Lys
			20					25				30			

Pro	Phe	Val	Ala	Cys	Ala	Glu	Cys	Gly	Phe	Pro	Val	Cys	Lys	Pro	Cys
		35					40					45			

Tyr	Glu	Tyr	Glu	Arg	Ser	Glu	Gly	Thr	Gln	Cys	Cys	Pro	Gln	Cys	Asn
					50				55		60				

Thr	Arg	Tyr	Lys	Arg	His	Lys	Gly	Cys	Pro	Arg	Val	Glu	Gly	Asp	Glu
					65			70		75				80	

Asp	Asp	Gly	Gly	Asp	Met	Asp	Asp	Phe	Glu	Glu	Glu	Phe	Gln	Ile	Lys
							85		90				95		

Ser	Pro	Thr	Lys	Gln	Lys	Pro	Pro	His	Glu	Pro	Val	Asn	Phe	Asp	Val
			100					105				110			

Tyr	Ser	Glu	Asn	Gly	Glu	Gln	Pro	Ala	Gln	Lys	Trp	Arg	Pro	Gly	Gly
			115					120			125				

Pro	Ala	Leu	Ser	Ser	Phe	Thr	Gly	Ser	Val	Ala	Gly	Lys	Asp	Leu	Glu
						130			135			140			

Gln	Glu	Arg	Glu	Met	Glu	Gly	Gly	Met	Glu	Trp	Lys	Asp	Arg	Ile	Asp
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Lys Trp Lys Thr Lys Gln Glu Lys Arg Gly Lys Leu Asn Arg Asp Asp
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 Ser Asp Asp Asp Asp Asp Lys Asn Asp Asp Glu Tyr Met Leu Leu Ala
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 Glu Ala Arg Gln Pro Leu Trp Arg Lys Val Pro Ile Pro Ser Ser Lys
 195 200 205
 Ile Asn Pro Tyr Arg Ile Val Ile Val Leu Arg Leu Val Val Leu Cys
 210 215 220
 Phe Phe Leu Lys Phe Arg Ile Thr Thr Pro Ala Met Asp Ala Val Pro
 225 230 235 240
 Leu Trp Leu Ala Ser Val Ile Cys Glu Leu Trp Phe Ala Leu Ser Trp
 245 250 255
 Ile Leu Asp Gln Leu Pro Lys Trp Ser Pro Val Thr Arg Glu Thr Tyr
 260 265 270
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 275 280 285
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 Pro Pro Ile Ile Thr Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp
 305 310 315 320
 Tyr Pro Val Asp Arg Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ser
 325 330 335
 Met Leu Leu Phe Asp Thr Leu Ser Glu Thr Ala Glu Phe Ala Arg Arg
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 Trp Val Pro Phe Cys Lys Lys Phe Thr Ile Glu Pro Arg Ala Pro Glu
 355 360 365
 Phe Tyr Phe Ser Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val Gln Pro
 370 375 380
 Thr Phe Val Lys Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe
 385 390 395 400
 Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Lys Pro Glu
 405 410 415
 Glu Gly Trp Val Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Thr
 420 425 430

Arg Asp His Pro Gly Met Ile Gln Val Tyr Leu Gly Ser Gln Gly Ala
435 440 445

Leu Asp Val Glu Gly Ser Glu Leu Pro Arg Leu Val Tyr Val Ser Arg
450 455 460

Glu Lys Arg Pro Gly Tyr Asn His His Lys Lys Ala Gly Ala Met Asn
465 470 475 480

Ser Leu Val Arg Val Ser Ala Val Leu Thr Asn Ala Pro Phe Ile Leu
485 490 495

Asn Leu Asp Cys Asp His Tyr Val Asn Asn Ser Lys Ala Val Arg Glu
500 505 510

Ala Met Cys Phe Leu Met Asp Lys Gln Leu Gly Lys Lys Leu Cys Tyr
515 520 525

Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg His Asp Arg Tyr
530 535 540

Ala Asn Arg Asn Thr Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp
545 550 555 560

Gly Ile Gln Gly Pro Val Tyr Val Gly Thr Gly Thr Val Phe Asn Arg
565 570 575

Gln Ala Leu Tyr Gly Tyr Asp Pro Pro Arg Pro Glu Lys Arg Pro Lys
580 585 590

Met Thr Cys Asp Cys Trp Pro Ser Trp Cys Cys Cys Cys Cys Cys Phe
595 600 605

Gly Gly Gly Lys Arg Gly Lys Ser His Lys Asn Lys Lys Gly Gly Gly
610 615 620

Gly Gly Glu Gly Gly Leu Asp Glu Pro Arg Arg Gly Leu Leu Gly
625 630 635 640

Phe Tyr Lys Lys Arg Ser Lys Lys Asp Lys Leu Gly Gly Gly Ala Ala
645 650 655

Ser Leu Ala Gly Gly Lys Lys Gly Tyr Arg Lys His Gln Arg Gly Phe
660 665 670

Glu Leu Glu Glu Ile Glu Glu Gly Leu Glu Gly Tyr Asp Glu Leu Glu
675 680 685

Arg Ser Ser Leu Met Ser Gln Lys Ser Phe Glu Lys Arg Phe Gly Gln
690 695 700

Ser Pro Val Phe Ile Ala Ser Thr Leu Val Glu Asp Gly Gly Leu Pro

705	710	715	720
Gln Gly Ala Ala Ala Asp Pro Ala Ala Leu Ile Lys Glu Ala Ile His			
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740 745 750			
Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys			
755 760 765			
Met His Cys Arg Gly Trp Lys Ser Val Tyr Cys Thr Pro Ala Arg Ala			
770 775 780			
Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu His Gln			
785 790 800			
val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Phe Met Ser Arg His			
805 810 815			
Cys Pro Leu Trp Tyr Ala Tyr Gly Gly Arg Leu Lys Trp Leu Glu Arg			
820 825 830			
Phe Ala Tyr Thr Asn Thr Ile Val Tyr Pro Phe Thr Ser Ile Pro Leu			
835 840 845			
Leu Ala Tyr Cys Thr Ile Pro Ala Val Cys Leu Leu Thr Gly Lys Phe			
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Ile Ile Pro Thr Leu Asn Asn Leu Ala Ser Ile Trp Phe Ile Ala Leu			
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Phe Leu Ser Ile Ile Ala Thr Gly Val Leu Glu Leu Arg Trp Ser Gly			
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Asp Glu Thr Asp Ala Phe Gly Glu Leu Tyr Leu Phe Lys Trp Thr Thr			
945 950 955 960			
Leu Leu Val Pro Pro Thr Thr Leu Ile Ile Ile Asn Met Val Gly Ile			
965 970 975			
Val Ala Gly Val Ser Asp Ala Val Asn Asn Gly Tyr Gly Ser Trp Gly			
980 985 990			

Pro Leu Phe Gly Lys Leu Phe Phe Ser Phe Trp Val Ile Leu His Leu
995 1000 1005

Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg Thr Pro
1010 1015 1020

Thr Ile Val Val Leu Trp Ser Ile Leu Leu Ala Ser Ile Phe Ser
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Leu Val Trp Val Arg Ile Asp Pro Phe Ile Pro Lys Pro Lys Gly
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Pro Val Leu Lys Pro Cys Gly Val Ser Cys
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<210> 39
<211> 2820
<212> DNA
<213> Oryza sativa

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gtcaccatgg ccagccaact cagcgcatac caggatgaag gagttcatgc caggactatg	360
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aagaacaagc tcacaccta cagggcagta atcattatgc gtctggtagt tctggggctc	660
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<210> 40

<211> 939

<212> PRT

<213> Oryza sativa

<400> 40

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Ala Ala Cys Arg Ala Cys Ser Tyr Ala Leu Cys Lys Ala Cys Leu Asp
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Glu Asp Ala Ala Glu Gly Arg Thr Thr Cys Ala Arg Cys Gly Gly Glu
 35 40 45
 Tyr Gly Ala Pro Asp Pro Ala His Gly Gln Gly Ala Val Val Glu Glu
 50 55 60
 Glu Val Glu Glu Ser His Glu Pro Ala Ala Gly Gly Val Arg Glu Arg
 65 70 75 80
 Val Thr Met Ala Ser Gln Leu Ser Asp His Gln Asp Glu Gly Val His
 85 90 95
 Ala Arg Thr Met Ser Thr His Ala Arg Thr Ile Ser Ser Val Ser Gly
 100 105 110
 Val Gly Ser Glu Leu Asn Asp Glu Ser Gly Lys Pro Ile Trp Lys Asn
 115 120 125
 Arg Val Glu Ser Trp Lys Glu Lys Lys Glu Lys Lys Ala Ser Ala
 130 135 140
 Lys Lys Ala Ala Ala Lys Ala Gln Ala Pro Pro Val Glu Glu Gln Ile
 145 150 155 160
 Met Asp Glu Lys Asp Leu Thr Asp Ala Tyr Glu Pro Leu Ser Arg Ile
 165 170 175
 Ile Pro Ile Ser Lys Asn Lys Leu Thr Pro Tyr Arg Ala Val Ile Ile
 180 185 190
 Met Arg Leu Val Val Leu Gly Leu Phe Phe His Tyr Arg Ile Thr Asn
 195 200 205
 Pro Val Tyr Ser Ala Phe Gly Leu Trp Met Thr Ser Val Ile Cys Glu
 210 215 220
 Ile Trp Phe Gly Phe Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp Cys
 225 230 235 240
 Pro Ile Asn Arg Glu Thr Tyr Val Asp Arg Leu Ile Ala Arg Tyr Gly
 245 250 255
 Asp Gly Glu Asp Ser Gly Leu Ala Pro Val Asp Phe Phe Val Ser Thr
 260 265 270
 Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala Asn Thr Val Leu
 275 280 285
 Ser Ile Leu Ala Val Asp Tyr Pro Val Glu Lys Ile Ser Cys Tyr Val
 290 295 300
 Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu Ser Leu Ala Glu Thr

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325	330	335	
Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ser Gln Lys Ile Asp Tyr Leu			
340	345	350	
Lys Asp Lys Ile His Pro Ser Phe Val Lys Glu Arg Arg Ala Met Lys			
355	360	365	
Arg Asp Tyr Glu Glu Tyr Lys Val Arg Ile Asn Ala Leu Val Ala Lys			
370	375	380	
Ala Gln Lys Thr Pro Glu Glu Gly Trp Ile Met Gln Asp Gly Thr Pro			
385	390	395	400
Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met Ile Gln Val Phe			
405	410	415	
Leu Gly Glu Thr Gly Ala Arg Asp Phe Asp Gly Asn Glu Leu Pro Arg			
420	425	430	
Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Gln His His Lys			
435	440	445	
Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr			
450	455	460	
Asn Ala Pro Tyr Ile Leu Asn Leu Asp Cys Asp His Tyr Val Asn Asn			
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Ser Lys Ala Val Arg Glu Ala Met Cys Phe Met Met Asp Pro Ser Val			
485	490	495	
Gly Arg Asp Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile			
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Asp Arg Ser Asp Arg Tyr Ala Asn Arg Asn Val Val Phe Phe Asp Val			
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Asn Met Lys Gly Leu Asp Gly Leu Gln Gly Pro Val Tyr Val Gly Thr			
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Gly Cys Cys Phe Tyr Arg Gln Ala Leu Tyr Gly Tyr Gly Pro Pro Ser			
545	550	555	560
Leu Pro Ala Leu Pro Lys Ser Ser Val Cys Ser Trp Cys Cys Cys			
565	570	575	
Cys Pro Lys Lys Lys Ala Glu Lys Ser Glu Lys Glu Met His Arg Asp			
580	585	590	

Ser Arg Arg Glu Asp Leu Glu Ser Ala Ile Phe Asn Leu Arg Glu Ile
 595 600 605
 Asp Asn Tyr Asp Glu Tyr Glu Arg Ser Met Leu Ile Ser Gln Met Ser
 610 615 620
 Phe Glu Lys Ser Phe Gly Leu Ser Ser Val Phe Ile Glu Ser Thr Leu
 625 630 635 640
 Met Glu Asn Gly Gly Val Pro Glu Ser Ala Asn Pro Ser Thr Leu Ile
 645 650 655
 Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Glu Lys Thr Glu
 660 665 670
 Trp Gly Lys Glu Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Phe
 675 680 685
 Leu Ser Arg His Cys Pro Leu Trp Tyr Gly Tyr Gly Gly Arg Leu
 690 695 700
 Lys Trp Leu Gln Arg Leu Ser Tyr Ile Asn Thr Ile Val Tyr Pro Phe
 705 710 715 720
 Thr Ser Leu Pro Leu Ile Ala Tyr Cys Cys Leu Pro Ala Ile Cys Leu
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 740 745 750
 Trp Phe Leu Gly Leu Phe Ile Ser Ile Ile Val Thr Ser Val Leu Glu
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 Leu Arg Trp Ser Gly Ile Gly Ile Glu Asp Trp Trp Arg Asn Glu Gln
 770 775 780
 Phe Trp Val Ile Gly Gly Val Ser Ala His Leu Phe Ala Val Phe Gln
 785 790 795 800
 Gly Ile Leu Lys Met Ile Ala Gly Leu Asp Thr Asn Phe Thr Val Thr
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 Ala Lys Ala Thr Asp Asp Thr Glu Phe Gly Glu Leu Tyr Val Phe Lys
 820 825 830
 Trp Thr Thr Val Leu Ile Pro Pro Thr Ser Ile Leu Val Leu Asn Leu
 835 840 845
 Val Gly Val Val Ala Gly Phe Ser Asp Ala Leu Asn Ser Gly Tyr Glu
 850 855 860

Ser Trp Gly Pro Leu Phe Gly Lys Val Phe Phe Ala Met Trp Val Ile
865 870 875 880

Met His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg
885 890 895

Thr Pro Thr Ile Val Val Leu Trp Ser Val Leu Leu Ala Ser Val Phe
900 905 910

Ser Leu Leu Trp Val Lys Ile Asp Pro Phe Ile Gly Ser Ser Glu Thr
915 920 925

Thr Thr Thr Asn Ser Cys Ala Asn Phe Asp Cys
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<211> 3168
<212> DNA
<213> Oryza savita

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Gln Cys Lys Thr Arg Tyr Lys Arg Leu Lys Gly Ser Pro Arg Val Pro
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 <212> DNA
 <213> Eucalyptus grandis

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 <212> DNA
 <213> Citrus mitis

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<211> 598
<212> DNA
<213> Zea mays

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<210> 83
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 <212> DNA
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	ctcccgtccg	ccccgccgat	cgaacagcca	ccgctcacct	ctcccacccg	ccaaaaacct	660
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	cacc						724